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Data Paper

DNA metabarcoding data from faecal samples of the lesser (*Myotis blythii*) and the greater (*Myotis myotis*) mouse-eared bats from Bulgaria

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Abstract

A comprehensive understanding of trophic interactions in terrestrial ecosystems is crucial for ecological research and conservation. Recent advances in non-invasive methods, such as environmental DNA (eDNA) metabarcoding, have enabled researchers to collect vast amounts of data on wild animal diets. However, sharing this data and metadata effectively and transparently presents new challenges. To address this, a new type of scholarly journal publication has emerged that aims to describe datasets rather than report research investigations. In this paper, we present a dataset of consumed prey species and parasites based on the metabarcoding of 113 faecal samples from the greater and lesser mouse-eared bats (*Myotis myotis* and *Myotis blythii*), along with a detailed description of the data sampling, laboratory analysis, and bioinformatics pipeline. Our dataset comprises 1018 unique Barcode Index Numbers (BINs) from 12 Classes and 43 Orders. In addition, we provide interactive Krona charts to visually summarize the taxonomic relationships and relative read abundance of the consumed prey species and parasites. This data can be used for meta-analysis, exploring new predator-prey and host-parasite interactions, studying inter- and intraspecific ecological interactions, and informing protected area management, among other applications. By sharing this dataset, we hope to encourage other researchers to use it to answer additional ecological questions and advance our understanding of trophic interactions in terrestrial ecosystems.

Key words: Bats (Chiroptera), metabarcoding, *Myotis myotis*, *Myotis blythii*, parasite-host interactions, predator-prey interactions

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Overview and background

Bats play a crucial role in terrestrial ecosystems worldwide by occupying various ecological niches and exploiting a range of food sources including insects, vertebrates, blood, nectar, pollen and fruit (Simmons 2005; Kunz et al. 2011). Due to their ecological abundance, bats could be used as bioindicator species that provide quantitative information on the quality of ecosystems, enabling the tracking of environmental alterations (Russo et al. 2021). Therefore, high-quality and de-

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tailed information on the diets of bat species in areas of conservation importance is essential. Historically, bat diets have been studied through the morphological analysis of invasively collected gut content or of noninvasively collected faeces (Whitaker et al. 2009). These morphological methods are time-consuming, require specialized entomological knowledge, and often can only identify prey down to order level. In recent years, advances in DNA barcoding and metabarcoding using high-throughput sequencing revolutionized the study of animal diets by providing a powerful, accurate, and time- and cost-efficient tool that can often identify prey down to the species level. As a consequence, after 2012 metabarcoding became increasingly popular (Ando et al. 2020). However, the methodology is still developing, and mistakes can occur at any level from sample collection, through PCR amplification and the bioinformatics pipeline, to data interpretation (Alberdi et al. 2018; O'Rourke et al. 2020). Thus, the sharing of transparent, detailed and open protocols and data is crucial for promoting good practices and avoiding errors. Here, we provide the full methods for collecting, metabarcoding, and analyzing a dataset of faecal samples collected from the greater and the lesser mouse-eared bats (*Myotis myotis* and *Myotis blythii*) in Bulgaria.

Myotis myotis (Borkhausen, 1797) and *Myotis blythii* s.l. (Tomes, 1857; for summary and discussion on taxonomy and phylogeny of the species see Ruedi 2020), family Vespertilionidae, are closely related sibling bat species that coexist in parts of Europe and the Middle East. While both are listed as Least Concerned in IUCN (Coroiu et al. 2016; Juste and Paunović 2016), in Europe they are protected under the Agreement on the Conservation of Populations of European Bats (EUROBATS). In Bulgaria, both species are listed as Near Threatened in the Red List of Protected Species of the country (Golemanski and Peev 2015). On the Balkan Peninsula, both bat species live almost exclusively in caves, or on rare occasions in mines, where they form mixed maternity and hibernation colonies. Interspecific competition is avoided mainly by habitat selection and different foraging strategies (Arlettaz 1999). *M. myotis* predominantly forages in forests and agricultural land with open, accessible ground (Arlettaz 1999; Stidsholt et al. 2023). *M. blythii*, in contrast, tends to forage in steppe-like habitats with dense grass and small shrubs (Arlettaz 1999). Both species use echolocation for aerial hunting as well as passive listening for gleaning prey off the ground and vegetation (Arlettaz et al. 2001; Siemers and Güttinger 2006; Stidsholt et al. 2023). However, when gleaning, *M. myotis* listens for the rustling sounds of large walking prey (Siemers and Güttinger 2006) while *M. blythii* eavesdrops on the mating song of bushcrickets (Jones et al. 2011).

The diet of *M. myotis* is extensively studied throughout its range with morphological methods (Audet 1990; Beck 1995; Arlettaz et al. 1997a, b; Arlettaz 1999; Pereira et al. 2002; Zahn et al. 2006; Steck and Güttinger 2006; Graclik and Wasielewski 2012), while less is known about the diet of *M. blythii* (Arlettaz et al. 1997a, b; Arlettaz 1999). These studies cover well the geographical and ecological variation in the diet of the two bat species, but they have a low taxonomic resolution and mostly identify prey only down to the order. Recent metabarcoding studies provided higher taxonomic resolution, however, only two studies investigated the diet of *M. myotis* (Galan et al. 2018; Alberdi et al. 2020), and only one study the diet of *M. blythii* (Mata et al. 2021), which additionally sampled and analyzed both species as one species complex due to methodological limitations.

Here, we provide a detailed description of the metabarcoding analysis of the faeces and of the diet of 113 individual bats (60 *M. myotis* and 53 *M. blythii*) col-

lected in an area with high biodiversity value (Cimatti et al. 2021). The dataset contains 1018 Barcode Index Numbers (BIN) species from 12 classes and 43 orders, ranging from prey species to various ecto- and endo-parasites (including mites, fleas, tapeworms, roundworms, and others). The BIN System clusters sequences using well established algorithms to produce operational taxonomic units that closely correspond to species. Interestingly, the presence of molluscan and annelid species (such as *Pomatias rivulare*, *Lumbricus rubellus*, and *Eisenia fetida*) suggests that the data could contain information on further trophic interactions from prey species of predatory carabid beetles or other arthropods, that in turn have been consumed by the bats. The re-using potential of our data set varies from meta-analysis of the diets of insectivorous bats to investigations of predator-prey or host-parasite interactions and interspecific food webs and ecological interactions, and to the management of protected areas.

In summary, the dataset we present in this paper is a valuable resource that can aid in advancing ecological research and conservation efforts. We hope that by sharing our data, we can contribute to a more collaborative and transparent research environment that will lead to more effective conservation and management of terrestrial ecosystems.

Methods

Sampling

Geographic coverage

Faecal samples were collected from individual bats at the entrance of the Orlova Chucka cave, Pepelina, Dve Mogili District, Bulgaria (43.593240, 25.960108). The cave is inhabited by 15 bat species all year round. In summer, however, it is predominantly occupied by mixed maternity colonies of *M. myotis* and *M. blythii*, as well as *Rhinolophus euryale* and *Rhinolophus mehelyi* (Borissov 2010). Mouse-eared bats are highly mobile with a hunting range of about 23 km around the cave (Egert-Berg et al. 2018; Stidsholt et al. 2023). While we collected the faecal samples at the cave entrance, our effective sampling area thus matches the foraging area of the bats, covering an area of approximately 1600 km^2 (Fig. 1A). Notably, a large proportion of the foraging grounds of the bats are in protected areas including NATURA 2000 sites and the Rusenski Lom Natural Park (Borissov 2010). The preferred foraging sites of the mouse-eared bats in the study area consist of small-scale agricultural areas, forests, open grasslands, karstic areas and riverine habitats (Fig. 1B–D).

Temporal coverage

Samples were collected from June to August in 2017 and 2018. Our period covers the lactation and post-lactation period of the female bats, during which they have to forage more actively to provide enough nutrition to both themselves and the pup.

Sampling methodology

Bats were captured in the morning (when returning to the roost after foraging) with a harp trap placed in front of the cave entrance. We emptied the trap

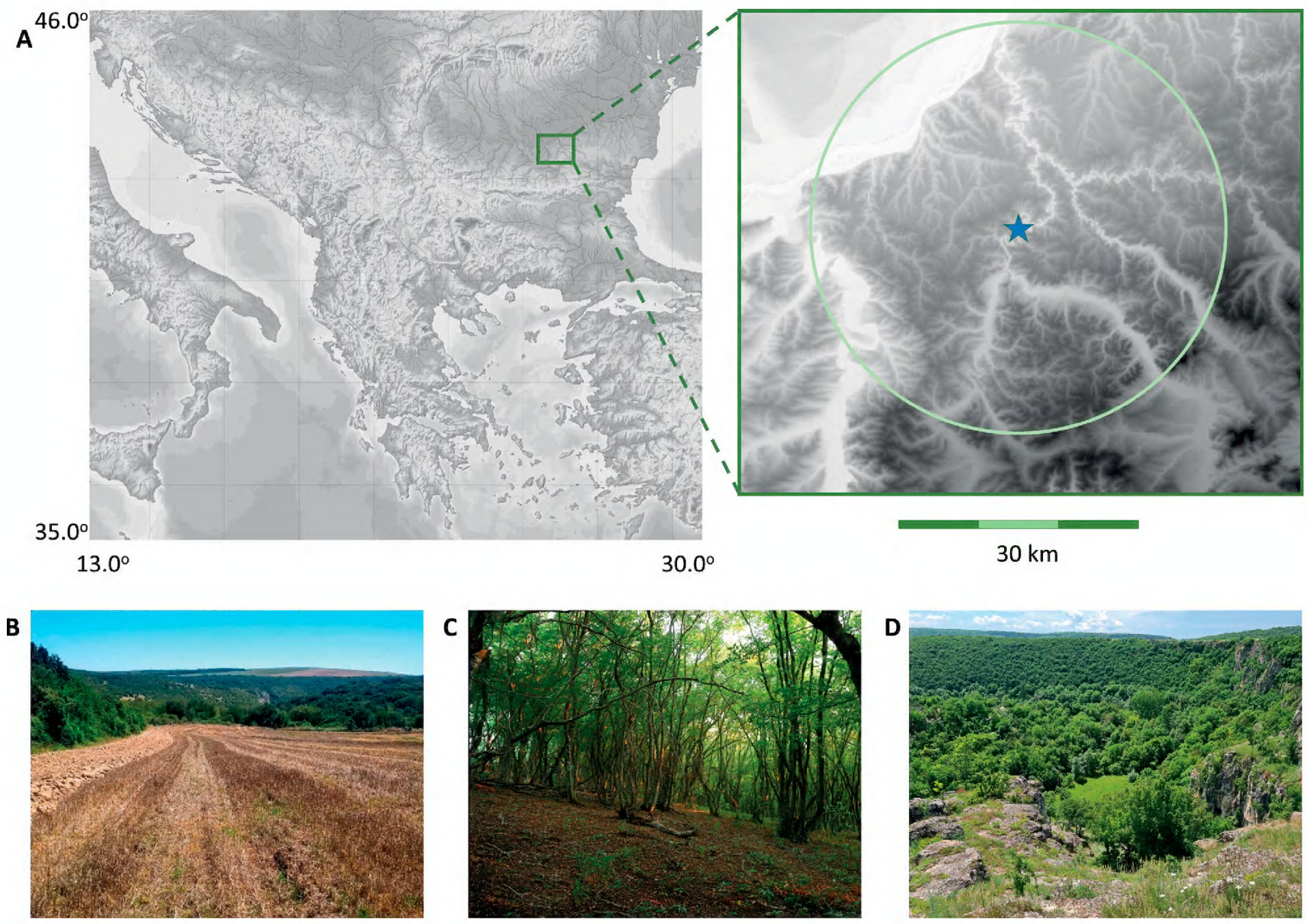

Figure 1. Geographic coverage, sampling area and typical hunting habitats **A** topographical map showing the study area with the sampling site marked by a star and the approximate foraging range of the bats represented by a circle **B–D** representative hunting habitats of the lesser and greater mouse-eared bats, including small-scale agricultural fields, forests, karstic areas, and riverine habitats (modified after Stidsholt et al. 2023).

every 5 to 10 minutes to minimize defecation in the trap, and thus potential cross-contamination between individuals by faeces attached to the fur. However, we could not fully prevent bats from defecating in the trap, therefore, a small proportion of cross-contamination between the different individuals might have occurred. After being removed from the trap, bats were placed in individual cotton bags until they defecated. Prior to data collection, the bags were brushed from previous guano and washed at 90 °C with bleach. After the bats had defecated in the bags, they were measured, sexed and identified to species level following Dietz and von Helversen (2004). To avoid misidentification, however, we used a conservative approach and only sampled individuals that could be clearly identified based on morphological measurements, identifying individuals as *M. myotis* if the length of the upper jaw (i.e., from the canine to the third molar, CM^3) was >9.4 mm and the forearm length (FA) >61 mm, and as *M. blythii* for CM^3 <9.0 mm and FA <59 mm. The guano pellets were placed in 2 ml Eppendorf tubes with 98% ethanol, which were subsequently stored in a freezer at -18 °C until further treatment. Bat catching and sample collection were performed under a permit granted by the Ministry of Environment and Waters, Bulgaria and under the control of the Regional Environment and Water Inspection Ruse (permit number 696/19.01.2017).

Laboratory procedures

DNA extraction, amplification, and metabarcoding

DNA metabarcoding was conducted at the AIM Lab (AIM—Advanced Identification Methods GmbH, Leipzig, Germany). Genomic data was extracted using the Quick-DNA Fecal/Soil Microbe 96 Kit (Zymo Research Corporation, Irvine CA, USA) and following the manufacturer's instructions. To control for artifacts arising from lab contamination, we ran 6 empty vials as negative control samples through the lab procedure: 2 before extraction, and 2 before each of the two rounds of PCR. These negative control samples were processed in the same way as the faecal samples. Further laboratory analyses were carried out as per the methods described in Uhler et al. (2022) using high-throughput sequencing (HTS)-adapted mini-barcode primers (mlCOIintF, dgHCO, Leray et al. 2013) targeting the mitochondrial CO1-5P region. HTS was performed on an Illumina MiSeq (Illumina Inc., San Diego, USA) "v3 chemistry" (2 × 300 base pairs, 600 cycles, maximum of 25 million paired end reads).

Bioinformatics

Preprocessing of raw Illumina reads

From each sample, paired-end reads were merged using the *-fastq_mergepairs* utility of USEARCH v11.0.667 (Edgar 2010) with the following parameters: *-fastq_maxdiffs* 99, *-fastq_pctid* 75, *-fastq_trunctail* 0. Next, adapter sequences were removed using CUTADAPT (Martin 2011) (single-end mode, with default parameters). Reads that did not contain the appropriate adapter sequences were filtered out in this step using CUTADAPT's *--discard-untrimmed* option. The remaining pre- processing steps (quality filtering, dereplication, chimera filtering, and clustering) were carried out using the VSEARCH suite v2.9.1 (Rognes et al. 2016).

Quality filtering was performed using *--fastq_filter*, allowing a maximum of 1 expected error along the length of the sequence and a minimum read length of 300 bases (parameters: *--fastq_maxee* 1, *--minlen* 300). This was followed by dereplication on the sample level using *--derep_fulllength*, keeping only a single copy of each unique sequence (parameters: *--sizeout*, *--relabel Uniq*). Cleaned and dereplicated sample files were concatenated into one large FASTA file, which was then dereplicated again, and also filtered for sequences occurring only once in the entire dataset (singletons) with the parameters *--minuniquesize* 2, *--sizein*, *--sizeout*, *--fasta_width* 0.

To save processing power, a clustering step (at 98% identity) was employed before chimera filtering using the VSEARCH utility *--cluster_size* and the centroids algorithm (parameters: *--id* 0.98, *--strand plus*, *--sizein*, *-- sizeout*, *--fasta_width* 0, *--centroids*). Chimeric sequences were then detected and filtered out from the resulting file using the VSEARCH *-- uchime_denovo* utility (parameters: *--sizein*, *--sizeout*, *--fasta_width* 0, *-- nonchimeras*). Next, a perl script obtained from the authors of VSEARCH (https://github.com/torognes/vsearch/wiki/VSEARCH-pipeline) was used to regenerate the concatenated FASTA file, but without the subsequently detected chimeric sequences. The resulting chimera-filtered file was then used to cluster the reads into operational taxonomic

units (OTUs) using SWARM v.3.1.0 (Mahé et al. 2022, parameters: *-d*13 *-z*). The value for the *d* parameter was chosen based on the results for the mitochondrial cytochrome *c* oxidase subunit I (COI) mini-barcode (Leray et al. 2013) from *in silico* experiments performed by Antich et al. (2021). The representative sequences of each OTU cluster were then sorted using VSEARCH (parameters: *--fasta_width* 0 *-- sortbysize*). An OTU table was constructed from the resulting FASTA file using the VSEARCH utility *--usearch_global* (parameters: *--strand plus -- sizein --sizeout --fasta_width* 0).

To reduce the risk of false positives, a cleaning step was employed that excluded read counts in the OTU table constituting <0.01% of the total number of reads in the sample. OTUs were additionally removed from the results based on negative control samples. If the number of reads for the OTU in any sample was less than the maximum for that OTU among negative controls, those reads were excluded from further analysis.

BLAST, reference database construction, and annotation

OTU representative sequences were blasted with the program Megablast (parameters: maximum hits: 1; scoring (match mismatch): 1–2; gap cost (open extend): linear; max E-value: 10; word size: 28; max target seqs 100) against (1) a custom database downloaded from GenBank (a local copy of the NCBI nucleotide database downloaded from ftp://ftp.ncbi.nlm.nih.gov/blast/db/), and (2) a custom database built from data downloaded from BOLD (www.boldsystems.org) (Ratnasingham and Hebert 2007, 2013) including taxonomy and BIN information. BLAST searches were performed using the GUI software suite Geneious (v.10.2.5 – Biomatters, Auckland, New Zealand).

All available Animalia data was downloaded from the BOLD database on 29 July 2022 using the available public data API (http://www.boldsystems.org/index.php/resources/api) in a combined TSV file format. The combined TSV file was then filtered to keep only the records that: (1) had a sequence (field 72, “nucleotides”); (2) had a sequence that did not hold exclusively one or more “-” (hyphens); had a sequence that did not contain non-IUPAC characters; (3) belonged to COI (the pattern “COI-5P” in either field 70 (“markercode”) or field 80 (“marker_codes”)); 5) had an available BIN (field 8, “bin_uri”). In (5), an exception was made in cases where the species belonging to that record did not occur with a BIN elsewhere in the dataset. In other words, “BIN-less” records were kept if their species were also completely BIN-less in the dataset. The dataset was then filtered to include only records from a custom European BOLD BLAST database.

Finally, a FASTA file annotated with (1) a Process ID (field 1, “processid”), (2) BIN (field 8), (3) taxonomy (fields 10, 12, 14, 16, 18, 20, 22 – “phylum_name”, “class_name”, “order_name”, “family_name”, “subfamily_name”, “genus_name”, “species_name”), (4) geolocation data (fields 47, 48, 55), and (5) GenBank ID (field 71, “genbank_accession”) was created from the filtered combined TSV file. This FASTA file was then converted into a BLAST database using Geneious v10.2.6 (Biomatters, Auckland, New Zealand). The results were exported and further processed according to methods described by Uhler et al. (2022).

Briefly, the resulting CSV files containing BLAST results were exported from Geneious and combined with the OTU table generated by the bioinformatic

pre-processing pipeline. The CSVs included: (1) OTU ID; (2) BOLD Process ID; (3) BIN; (4) Hit-%-ID value (the percentage of identical base pairs of the OTU query sequence with its closest counterpart in the reference database); (5) Grade-%-ID value (a value that combines query coverage, E-value and Hit-%-ID with weights of 0.5, 0.25 and 0.25 respectively); (6) length of the top BLAST hit sequence; (7) phylum, class, order, family, genus and species for each detected OTU.

As an additional measure of control other than BLAST, the OTUs were classified into taxa using the Ribosomal Database Project (RDP) naïve Bayesian classifier (Wang et al. 2007), which was trained on a cleaned COI dataset of Arthropods and Chordates (plus outgroups; see Porter and Hajibabaei 2018). OTUs were also annotated with the taxonomic information from the NCBI (downloaded from https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/), followed by the creation of a taxonomic consensus between BOLD, NCBI and RDP to facilitate assessment of the resulting matches across the three reference databases. To create the taxonomic consensus, we first adjusted the taxonomic depths of each hit from the three reference databases based on its Grade-%-ID value (>97% for species, >95% for genus, >90% for family, >85% for order, >80% for class, and >75% for phylum). In cases where a taxonomically identical match was found in all three reference databases (BOLD BLAST, NCBI BLAST, and RDP classifier), the OTUs were assigned the taxonomic score “A”. Where BOLD & NCBI agreed, but RDP disagreed, the OTUs were assigned the score “B”. This was in most cases the result of certain taxa either missing or not being represented with sufficient numbers in the RDP classifier’s training set. Finally, where NCBI & RDP agreed, but BOLD disagreed, the OTUs got the score “C”. A score of “C” commonly occurs in cases where BOLD cannot resolve a species due to a phenomenon commonly referred to as “BIN sharing”. For the purposes of constructing the consensus, in every case of a BIN that is shared between 2 or more species in the database, we disregarded the species-level information given by the BOLD BLAST result. In this way, we gave precedence to a species-level annotation with a score of “C” (by means of NCBI and RDP) over a hypothetical genus-level annotation with a score of “A”. We treated cases of identifications to different taxonomic levels across the three references in the same way, i.e., a lower score (consensus level) was preferred if it meant an increase to the taxonomic resolution.

BOLD taxonomy was then used to create Krona charts (Fig. 2). These interactive HTML charts were created by means of KronaTools v2.7 (Ondov et al. 2011) (https://github.com/marbl/Krona/wiki/KronaTools). Krona charts are a variation of a sunburst diagram, a pie-chart-like visualization, which is commonly used to plot hierarchical data in a way that emphasizes their taxonomic relationships and relative abundance. A Krona chart shows hierarchy through a series of concentric rings, where each ring corresponds to a level in the hierarchy, and each ring is segmented proportionally to represent read abundance. Where multiple OTUs were identified to the same taxon, read counts were summed over all those OTUs. A set of charts was created: one for each individual sample, one summed over all samples, as well as one each summed over *M. myotis*- or *M. blythii*-derived samples, respectively. First, a custom script was used to extract from the final Excel results table only the OTU table counts and associated taxonomic annotations. Then, intermediate sample count (.TAX) files for KronaTools were created using a bash script obtained

from https://github.com/GenomicaMicrob/OTUsamples2krona. The charts were created by the same script using the command "ktImportText [SAMPLE.TAX] -n SAMPLE -o SAMPLE.html".

Results and discussion

The presented dataset is a comprehensive collection of 1018 BIN species belonging to 12 Classes and 43 Orders. The interactive Krona charts, based on BOLD taxonomy, provide a useful tool for visualizing the dataset (Fig. 2). These charts present the proportions of the sequence counts of respective species/taxonomic groups relative to all counts. However, it is essential to acknowledge that the sequence counts obtained from the samples do not necessarily correspond to the biomass of the original sample due to inherent methodological limitations and considerable variability in species sizes (Elbrecht et al. 2017; Lamb et al. 2019). Therefore, the relative read abundance (RRA, Deagle et al. 2019) presented in the Krona charts should only be considered a visual guide to the taxonomic diversity and relative abundance of the reads, and not an indication of the actual consumed biomass of the respective species.

Insects made up the largest proportion of the detected species. The observed differences in the RRA from carabid beetles between *M. myotis* (46%) and *M. blythii* (7%) aligns with the differences in diet, foraging style and habitat of these species (Arlettaz et al. 1997a, b; Arlettaz 1999). However, the differences in the RRA of other taxa shown in the Krona charts were less pronounced between the two bat species, with an important exception being Orthoptera. In *M. myotis* samples, the majority of Orthopteran species belonged to the family Gryllidae (crickets), while in *M. blythii* samples, the records primarily came from the family Tettigoniidae (bush-crickets), including species such as *Tettigonia*, *Phaneroptera*, *Pholidoptera*, *Decticus*, *Poecilimon*, and *Isophya*. This observation aligns with the known differences in foraging strategies between the two species, where *M. myotis* primarily utilizes rustling sounds produced by crickets, while *M. blythii* eavesdrops on the mating songs of bush-crickets (Arlettaz et al. 1997b; Jones et al. 2011; Stidsholt et al. 2023).

Importantly, since the RRA does not accurately represent actual biomass abundance, it is crucial to complement this data with other research techniques, such as biologging (Stidsholt et al. 2023), behavioral experiments (Stat et al. 2019; Jones et al. 2020) and ecological studies (Evans et al. 2016; Sato et al. 2021; Andriollo et al. 2021), to enhance the reliability and scope of the results. For instance, Stidsholt et al. (2023) utilized miniature airborne tags attached to wild foraging *M. myotis* individuals from the same colony as used in this study. The number of attacks were identified and categorized as either aerial or ground captures. Out of 3917 recorded prey attacks, approximately two-thirds were ground attacks. The results revealed that nearly all ground attacks were triggered by rustling sounds from carabid beetles, while fewer than 1% of ground attacks were initiated by mating calls of bush-crickets. These additional findings help place the results of the metabarcoding analysis into a more biologically relevant context.

Notably, in addition to the bats' prey species, the provided dataset also includes reads from various ecto- and endo-parasites, such as ticks (*Ixodes*), mites (Mesostigmata and Sarcoptiformes), roundworms (Strongylida and

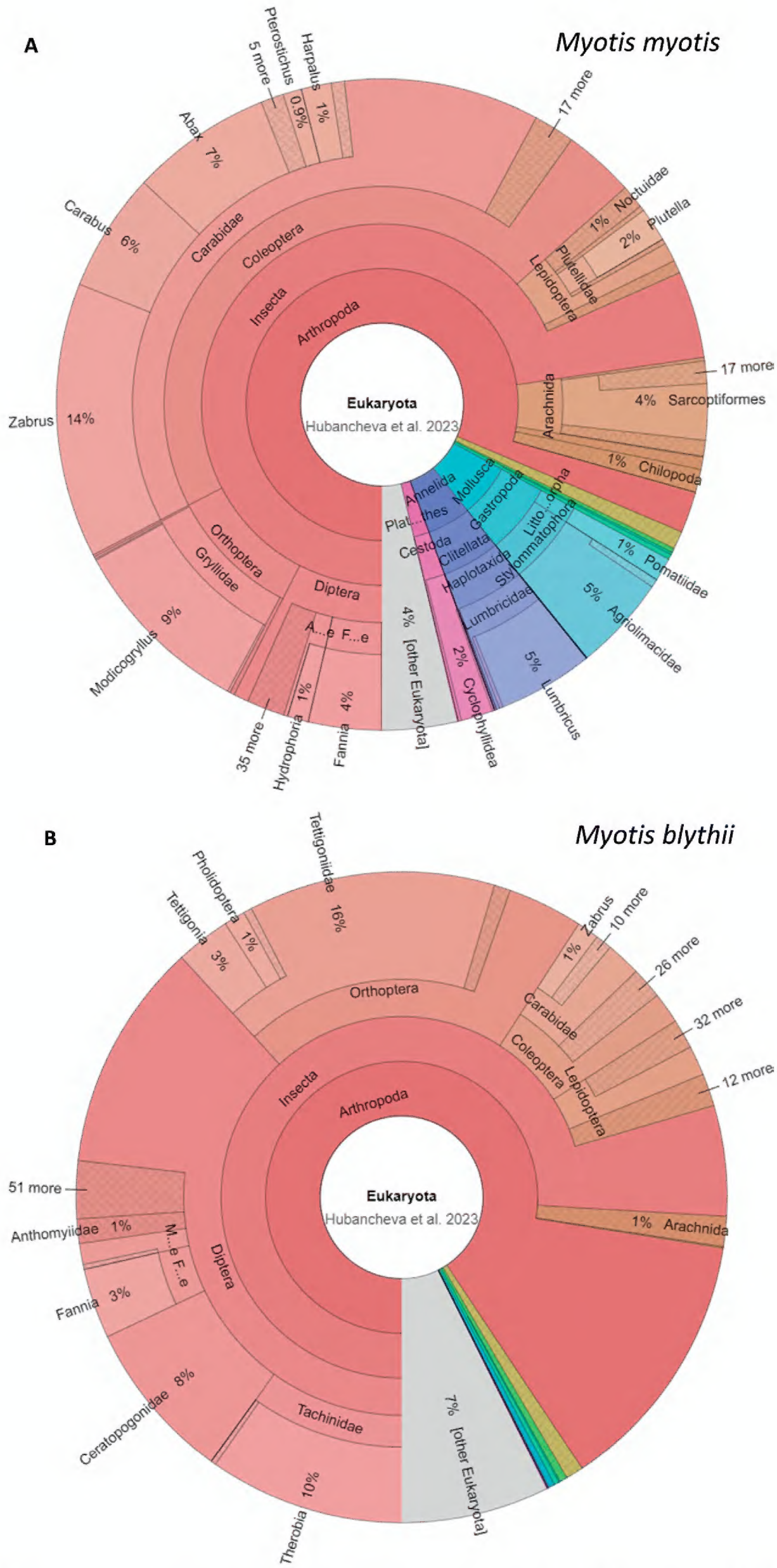

Figure 2. Taxonomic relationships and relative read abundance of prey and parasite species in faecal samples collected from **A** 60 individuals of the greater mouse-eared bat, *Myotis myotis*, and **B** 53 individuals of the lesser mouse-eared bat, *Myotis blythii*. The Krona charts presented in this figure exclude the reads from the two bat species. However, Krona charts with included bat reads can be found in the Supplementary Information. An interactive graph is also available in the online version of this publication, offering a more in-depth analysis of the data.

Rhabditida), and other parasite species. Furthermore, we identified molluscs (Gastropoda) and worms (Annelida) in the samples, including *Pomatias rivulare*, *Lumbricus rubellus*, and *Eisenia fetida*, which were likely consumed by predatory carabid beetles or other arthropods that were then consumed by the bats. Moreover, the presence of species from the roundworm genus *Steinernema*, which are known to parasitize mole crickets and other bat prey, suggests that the dataset also contains parasites of the bats' prey species. This comprehensive dataset thus offers valuable insights into the diversity and abundance of the parasites, the prey and their associated species of the greater and the lesser mouse-eared bats.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

A.H. – Conceptualization, A.H. V.B. – Data curation, A.H., V.B. – Formal Analysis, A.H., H.R.G. – Funding acquisition, A.H., V.B., J.M. – Methodology, A.H., H.R.G – Project administration, H.R.G. J.M. – Resources, V.B. – Software, H.R.G., J.M. – Supervision, A.H., V.B. – Validation, A.H., V.B. – Visualization, A.H., V.B. – Writing original draft, A.H., V.B., J.M., H.R.G. – Writing review & editing.

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Data availability

The dataset described in this data paper is available in the Supplementary materials and has been deposited in Dryad under https://doi.org/10.5061/dryad.4tmpg4fgz. The Dryad mirror also contains the raw metabarcoding reads from Illumina.

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Supplementary material 1

Metabarcoding data from *M. myotis* and *M. blythii* from Bulgaria

Authors: Antoniya Hubancheva, Vedran Bozicevic, Jérôme Morinière, Holger R. Goerlitz

Data type: metabarcoding in tabular format

Explanation note: An Excel file, titled "mmyotis-mblythii-metabarcoding-data-bulgaria.xlsx", includes DNA metabarcoding data from the faecal samples of the lesser (*Myotis blythii*) and greater (*Myotis myotis*) mouse-eared bats from Bulgaria and a second sheet that contains descriptions of the columns in the metabarcoding dataset, along with their meanings.

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Link: https://doi.org/10.3897/mbmg.7.106844.suppl1

Supplementary material 2

Taxonomic relationships and relative abundance of prey and parasite species in faecal samples from *M. myotis* and *M. blythii* from Bulgaria

Authors: Antoniya Hubancheva, Vedran Bozicevic, Jérôme Morinière, Holger R. Goerlitz

Data type: interactive chart

Explanation note: An interactive Krona chart that provides a visual representation of the metabarcoding data.

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